

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:17:05 ; Search time 26.4 Seconds
(without alignments)
43.677 Million cell updates/sec

Title: US-09-629-719D-8

Perfect score: 61

Sequence: 1 XPRGGSVLVTGC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 1579

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	45.9	11	2	S60354
2	26	42.6	7	4	S15597
3	24	39.3	10	2	A61131
4	24	39.3	12	2	A33900
5	23	37.7	11	2	YHRT
6	23	37.7	11	2	YHNU
7	23	37.7	11	2	YHBO
8	23	37.7	11	2	YHAE
9	23	37.7	11	2	YHUFHY
10	21	34.4	9	2	A60522
11	21	34.4	9	2	A29477
12	21	34.4	11	2	I65231
13	21	34.4	12	2	S70337
14	21	34.4	12	2	S43170
15	20	32.8	9	2	A26363
16	20	32.8	9	2	S27233
17	20	32.8	12	2	A49261
18	19	31.1	9	2	PC2197
19	19	31.1	10	2	A55695
20	19	31.1	12	2	A61309
21	19	31.1	12	2	S65629
22	19	31.1	12	2	PH0930
23	18	29.5	8	2	PT0530
24	18	29.5	9	2	B28495
25	18	29.5	9	2	S06375
26	18	29.5	9	2	B61364
27	18	29.5	11	2	PN0169
28	18	29.5	11	2	PT0218
29	18	29.5	12	2	S29479

30	18	29.5	12	2	PT0319	Ig heavy chain CRD
31	17	27.9	4	2	S47552	ubiquitin - rat
32	17	27.9	7	2	E61491	seed protein ws-5
33	17	27.9	8	2	PT0279	Ig heavy chain CRD
34	17	27.9	9	1	YFPG	thymic factor - pl
35	17	27.9	9	2	A60957	thymocyte growth p
36	17	27.9	10	2	E60589	sperm-activating p
37	17	27.9	10	2	S06964	hypothetical prote
38	17	27.9	11	2	E60691	phycobilisome 8k 1
39	17	27.9	11	2	PC2173	triacylglycerol 11
40	17	27.9	11	2	PH0947	T-cell receptor be
41	17	27.9	11	2	I52304	gene rsSR4 protei
42	17	27.9	11	2	A34243	H-hyosoporphin - ja
43	17	27.9	12	2	A60757	enterotoxin C-1 -
44	17	27.9	12	2	PH1606	Ig H chain V-D-J r
45	16	26.2	6	2	JU0355	lipopeptide WS1279

ALIGNMENTS

RESULT 1
S60354
retinal oxidase - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S60354
R:Huang, D.Y.; Ichikawa, Y.
Biochim. Biophys. Acta 1243, 431-436, 1995
A:Title: Identification of essential lysyl and cysteinyl residues, and the amino acid
A:Reference number: S60354; PMID:95244596
A:Accession: S60354
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <HQA>

Query Match 45.9%; Score 28; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GGSVLVTGC 12
DB 1 GGDVHTXGC 9

RESULT 2
S15597
orf 4 rara 5'-region - human
C:Species: Homo sapiens (man)
C>Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C:Accession: S15597
R:Brand, N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A:Title: Characterization of a functional promoter for the human retinoic acid recept
A:Reference number: S15594; PMID:91088249
A:Accession: S15597
A:Molecule type: DNA
A:Residues: 1-7 <BRA>
A:Cross-references: EMBL:X56058; NID:q35876
A:Note: this ORF from fig. 2 is not annotated in Genbank entry HSRARA2, release 111.0
C:Comment: This sequence is not thought to be translated.
C:Genetics:
A:Gene: GDB:RARA
A:Cross-references: GDB:120337; OMIM:180240
A:Map position: 17q12-17q12

Query Match 42.6%; Score 26; DB 4; Length 7;
Best Local Similarity 83.3%; Pred. No. 2.8e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 PRGGSV 7

Db 2 PRGCV 7
|||
RESULT 3
A61131
hydrin 2 - bullfrog
N:Alternate names: AVT-related peptide
C:Species: Rana catesbeiana (bullfrog)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Jul-1997
C:Accession: A61131
R:Iwamura, S.; Hayashi, H.; Yamashita, M.; Kikuyama, S.
Gen. Comp. Endocrinol. 84, 412-418, 1991
A:Title: Arginine vasotocin (AVT) and AVT-related peptide are major aldosterone-releasing
A:Reference number: A61131; MUID:9225310
A:Accession: A61131
Molecule type: protein
Residues: 1-10 <IYW>
Comment: Both the decapeptide (hydrin 2) and the amidated nonapeptide (Arg-vasotocin)
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; neuropeptide; pituitary
F:1-9/Product: Arg-vasotocin #status experimental <RVAS>
F:9/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glyc

Query Match 39.3%; Score 24; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRGS 5
|||
Db 7 PRGS 10

RESULT 4
A33900
hydrin 1 - African clawed frog
N:Alternate names: arginine-vasotocin-related peptide; vasotocinyl-Gly-Lys
C:Species: Xenopus laevis (African clawed frog)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 31-Mar-1997
C:Accession: A33900; S30176
R:Rouille, Y.; Michel, G.; Chauvet, M.T.; Chauvet, J.; Acher, R.
Proc. Natl. Acad. Sci. U.S.A. 86, 5272-5275, 1989
A:Title: Hydrins, hydroosmotic neurohypophyseal peptides: osmoregulatory adaptation in a
A:Reference number: A33900; MUID:89315779
A:Accession: A33900
Status: preliminary
Molecule type: protein
Residues: 1-12 <ROU>
R:Iwamura, S.; Hayashi, H.; Kikuyama, S.
Biochim. Biophys. Acta 1176, 143-147, 1993
A:Title: An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenop
A:Reference number: S30176; MUID:93200145
A:Accession: S30176
A:Molecule type: protein
A:Residues: 1-12 <IYW>
C:Keywords: neuropeptide

Query Match 39.3%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRGS 5
|||
Db 7 PRGS 10

RESULT 5
YHRT
morphogenetic neuropeptide - rat
C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co
A:Reference number: A93266; MUID:82035850
A:Accession: A01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; hypothalamus; intestine; neuropeptide; pyroglutam
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 37.7%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PRGSVLV 9
|||
Db 2 PRGSKVL 9

RESULT 6
YHNU
morphogenetic neuropeptide - human
C:Species: Homo sapiens (man)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B01427; A01427
R:Bodenmuller, H.; Schaller, H.C.
Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from co
A:Reference number: A93266; MUID:82035850
A:Accession: B01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Birr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; MUID:82050803
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuro
F:1/Modified site: blocked amino end (Gln) (probably pyroglutamate carboxylic acid) #st

Query Match 37.7%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PRGSVLV 9
|||
Db 2 PRGSKVL 9

RESULT 7
YHBO
morphogenetic neuropeptide - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: C01427; A01427
R:Bodenmuller, H.; Schaller, H.C.

Nature 293, 579-580, 1981
A:Title: Conserved amino acid sequence of a neuropeptide, the head activator, from coel
A:Reference number: A93266; PMID:82035850
A:Accession: C01427
A:Molecule type: protein
A:Residues: 1-11 <BOD>
R:Blirr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; PMID:82050803
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structu
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head
malian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: blocked amino end; growth factor; hormone; hypothalamus; intestine; neuropep
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu

Query Match 37.7%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRGGSVLV 9
| | | | :
Db 2 PRGGSKVI 9

RESULT 8
YHXA
morphogenetic neuropeptide - sea anemone (Anthopleura elegantissima)
N:Alternate names: head activator
C:Species: Anthopleura elegantissima
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A93900; A01427
R:Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981
A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A:Reference number: A93900
A:Accession: A93900
A:Molecule type: protein
A:Residues: 1-11 <SCH>
R:Blirr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; PMID:82050803
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical structu
C:Comment: This peptide was first isolated from nerve cells of hydra and was called head
a mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 37.7%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRGGSVLV 9
| | | | :
Db 2 PRGGSKVI 9

RESULT 9
YHJFHY
morphogenetic neuropeptide - Hydra attenuata
N:Alternate names: head activator
C:Species: Hydra attenuata
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: B93900; A01427
R:Schaller, H.C.; Bodenmuller, H.
Proc. Natl. Acad. Sci. U.S.A. 78, 7000-7004, 1981

A:Title: Isolation and amino acid sequence of a morphogenetic peptide from hydra.
A:Reference number: A93900
A:Accession: B93900
A:Molecule type: protein
A:Residues: 1-11 <SCH>
R:Blirr, C.; Zachmann, B.; Bodenmuller, H.; Schaller, H.C.
FEBS Lett. 131, 317-321, 1981
A:Title: Synthesis of a new neuropeptide, the head activator from hydra.
A:Reference number: A91296; PMID:82050803
A:Contents: annotation; synthesis
A:Note: the synthetic peptide was identical with the natural peptide in chemical stru
C:Comment: This peptide was first isolated from nerve cells of hydra and was called h
n mammalian intestine and hypothalamus.
C:Superfamily: unassigned animal peptides
C:Keywords: growth factor; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 37.7%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRGGSVLV 9
| | | | :
Db 2 PRGGSKVI 9

RESULT 10
A60522
sperm-activating peptide SAP-IV - sea urchin (Diadema setosum)
C:Species: Diadema setosum
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60522
R:Toshino, K.I.; Kurita, M.; Yamaguchi, M.; Nomura, K.; Takao, T.; Shimonishi, Y.; Su
Comp. Biochem. Physiol. B 95, 423-429, 1990
A:Title: A species-specific sperm-activating peptide from the egg jelly of the sea ur
A:Reference number: A60522; PMID:90227916
A:Accession: A60522
A:Molecule type: protein
A:Residues: 1-9 <YOS>
C:Superfamily: unassigned animal peptides
F:2-9/Disulfide bonds: #status experimental

Query Match 34.4%; Score 21; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 PRGGSV 7
| | | | :
Db 3 PWGAV 8

RESULT 11
A29477
diuretic neuropeptide F1 - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
C:Accession: A29477
R:Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schoo
Biochem. Biophys. Res. Commun. 149, 180-186, 1987
A:Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta
A:Reference number: A29477; PMID:88077077
A:Accession: A29477
A:Molecule type: protein
A:Residues: 1-9 <PRO>
A:Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of
C:Keywords: neuropeptide

Query Match 34.4%; Score 21; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 LVTGC 12
|:|
Db 2 LITMC 6

RESULT 12

I65231
CCK-B gastrin receptor isoform - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C:Accession: I65231
R:Miyaake, A.
Biochem. Biophys. Res. Commun. 208, 230-237, 1995
A:Title: A truncated isoform of human CCK-B/gastrin receptor generated by alternative splicing
C:Date: 152307; MUID:95194412
A:Accession: I65231
Status: preliminary; translated from GB/EMBL/DBJ
Molecule type: mRNA
Residues: 1-11 <RES>
A:Cross-references: GB:S76072; NID:g913752; PIDN:AAB33740.1; PID:g913753
C:Genetics:
A:Gene: CCK-B

Query Match 34.4%; Score 21; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 4 GGSVLY 9
|:|:|
Db 4 GGNNLI 9

RESULT 13

S70337
napin small chain S2 - Swedish turnip (fragment)
C:Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)
C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C:Accession: S70337
R:Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 23-33, 1996
A:Title: Purification and sequencing of multiple forms of Brassica napus seed napin small chain
A:Reference number: S70336; MUID:96283790
A:Accession: S70337
Status: preliminary
Molecule type: protein
Residues: 1-12 <NEU>

Query Match 34.4%; Score 21; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 PRGS 6
|:|:|
Db 5 PGGS 9

RESULT 14

S43170
kinesin light chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: S43170
R:Chernajovsky, Y.; Brown, A.; Jones, T.A.; Sheer, D.
Submitted to the EMBL Data Library, December 1992
A:Description: Promoter first exon/intron characterization and chromosomal location of the human kinesin light chain
A:Reference number: S43170
A:Accession: S43170
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <CHE>

A:Cross-references: EMBL:X69658; NID:g468786; PIDN:CAA49349.1; PID:g468787

Query Match 34.4%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RGGS 6
|:|:|
Db 3 RGGS 6

RESULT 15

A26363
cardioactive peptide - green crab (fragment)
C:Species: Carcinus maenas (green crab, common shore crab)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: A26363
R:Stangier, J.; Hilbich, C.; Beyreuther, K.; Keller, R.
Proc. Natl. Acad. Sci. U.S.A. 84, 575-579, 1987
A:Title: Unusual cardioactive peptide (CCAP) from pericardial organs of the shore crab
A:Reference number: A26363
A:Accession: A26363
A:Molecule type: protein
A:Residues: 1-9 <STA>

Query Match 32.8%; Score 20; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 TGC 12
|:|
Db 7 TGC 9

Search completed: October 10, 2002, 06:17:06
Job time: 252 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:21:20 ; Search time 17.65 Seconds
(without alignments)
26.325 Million cell updates/sec

Title: US-09-629-719D-8

Perfect score: 61
Sequence: 1 XPRGGSVLYVGC 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 463

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	37.7	11	1	MORN_HUMAN
2	21	34.4	9	1	DNFI_LOCHI
3	20	32.8	9	1	CCAP_CARMA
4	18	29.5	9	1	CONO_CONST
5	18	29.5	9	1	OXYT_CYPCA
6	18	29.5	11	1	NUHM_CANFA
7	17	27.9	9	1	THYE_PIG
8	17	27.9	12	1	VIAK_MSSV
9	16	26.2	8	1	RS7_MYCIT
10	16	26.2	11	1	TKNA_SCYCA
11	15	24.6	9	1	CONO_CONGE
12	15	24.6	9	1	MGMT_BOVIN
13	15	24.6	10	1	BRK_ONCMY
14	15	24.6	12	1	CXAI_CONIM
15	14	23.0	9	1	OXYR_RAJCL
16	14	23.0	9	1	SAP_STOYA
17	14	23.0	10	1	TKU3_LOCHI
18	14	23.0	11	1	CEPI_ACHFU
19	14	23.0	11	1	PKVI_PERAM
20	13.5	22.1	12	1	UR2B_CYPCA
21	13	21.3	7	1	CCFI_ENTFA
22	13	21.3	7	1	PAR5_HIRME
23	13	21.3	8	1	CAD1_ENTFA
24	13	21.3	8	1	UF06_MOUSE
25	13	21.3	9	1	ISOR_CYPCA
26	13	21.3	10	1	ESTR_SCYCA
27	13	21.3	10	1	PAP1_PARMA
28	13	21.3	10	1	TPIS_NICPL
29	13	21.3	10	1	URAI_HUMAN
30	13	21.3	11	1	BPP4_BOTIN
31	13	21.3	11	1	PKCI_CARMO
32	13	21.3	11	1	RE41_LITRU
33	13	21.3	12	1	PSF3_PHYPA

34	12	19.7	4	1	TUFT_HUMAN
35	12	19.7	7	1	LANC_CARUI
36	12	19.7	8	1	ALI6_CARUI
37	12	19.7	8	1	ALI9_CARMA
38	12	19.7	8	1	FAR7_ASCSU
39	12	19.7	8	1	LMP2_LOCHI
40	12	19.7	8	1	LPR_LEUMA
41	12	19.7	8	1	PPK2_PERAM
42	12	19.7	8	1	PPK3_PERAM
43	12	19.7	8	1	UC26_MAIZE
44	12	19.7	8	1	UPA1_HUMAN
45	12	19.7	8	1	UPAA_HUMAN

ALIGNMENTS

RESULT	ID	MORN_HUMAN	STANDARD:	PRT:	11 AA.
AC	P01163	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	01-OCT-1996 (Rel. 34, Last annotation update)				
DE	Morphogenetic neuroepitide (Head activator) (Ha).				
OS	Homo sapiens (Human)				
OS	Rattus norvegicus (Rat)				
OS	Bos taurus (Bovine)				
OS	Anthopleura elegantissima (Sea anemone), and				
OS	Hydra attenuata (Hydra) (Hydra vulgaris).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606, 10116, 9913, 6110, 6087;				
RN	[1]				
RP	SEQUENCE.				
RC	SPECIES=Human, Rat, and Bovine;				
RX	MEDLINE=82035850; PubMed=7290191;				
RA	Bodenmuller H., Schaller H.C.;				
RT	"Conserved amino acid sequence of a neuroepitide, the head activator,				
RT	from coelenterates to humans.";				
RL	Nature 293:579-580(1981).				
RN	[2]				
RP	SEQUENCE.				
RC	SPECIES=A. elegantissima, and H. attenuata;				
RA	Schaller H.C., Bodenmuller H.;				
RT	"Isolation and amino acid sequence of a morphogenetic peptide from				
RT	hydra.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 78:7000-7004(1981).				
RN	[3]				
RP	SYNTHESIS.				
RX	MEDLINE=82050803; PubMed=7297679;				
RA	Birr C., Zachmann B., Bodenmuller H., Schaller H.C.;				
RT	"Synthesis of a new neuroepitide, the head activator from hydra.";				
RL	FEBS Lett. 131:317-321(1981).				
RN	[4]				
RP	FUNCTION.				
RX	MEDLINE=90059923; PubMed=2583101;				
RA	Schaller H.C., Druffel-Augustin S., Dubel S.;				
RT	"Head activator acts as an autocrine growth factor for NH15-CA2 cells				
RT	in the G2/mitosis transition.";				
RL	EMBO J. 8:3311-3318(1989).				
CC	-1- FUNCTION: HA ACTS AS AN AUTOCRINE GROWTH FACTOR FOR NEURAL CELLS				
CC	IN THE G2/MITOSIS TRANSITION.				
CC	-1- CAUTION: THIS PEPTIDE WAS FIRST ISOLATED FROM NERVE CELLS OF HYDRA				
CC	AND WAS CALLED HEAD ACTIVATOR BY THE AUTHORS, BECAUSE IT INDUCED				
CC	HEAD-SPECIFIC GROWTH AND DIFFERENTIATION IN THIS ANIMAL. IT HAS				
CC	BEEN FOUND IN MAMMALIAN INTESTINE AND HYPOTHALAMUS.				
DR	PIR: B01427; YHNU.				
DR	PIR: A01427; YHRT.				
DR	PIR: C01427; YHBO.				
DR	PIR: A93900; YHXA.				
DR	PIR: B93900; YHGFY.				
KW	Growth factor; Cell cycle; Mitosis.				

FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA: 1142 MW: 37927417C325B878 CRC64;
Query Match 37.7%; Score 23; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 PROGSVLU 9
Db 2 PPGGSKVL 9
RESULT 2
DNFI_LOCOMI STANDARD; PRT: 9 AA.
ID DNFI_LOCOMI
AC P16339;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Locupressin (Diuretic neuropeptide FI/F2).
DE Locusta migratoria (Migratory locust).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Subesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
Delage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
Locusta migratoria.";
RT Locusta migratoria.";
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -1- FUNCTION: DIURETIC HORMONE.
CC -1- SUBUNIT: F2 IS AN ANTIPARALLEL DISULFIDE LINKED DIMER OF F1.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR: A29477; A29477.
DR InterPro: IPR000981; Neuropeptide_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN F1.
FT DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA: 976 MW: 56EB176EB451A057 CRC64;
Query Match 34.4%; Score 21; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 LVTCG 12
Db 2 LITNC 6
RESULT 3
CCAP_CARMA STANDARD; PRT: 9 AA.
ID CCAP_CARMA
AC P38556;
01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DE Cardioactive peptide (CCAP).
OS Carcinus maenas (Common shore crab) (Green crab),
Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
Tenebrio molitor (Yellow mealworm), and
OS Spodoptera eridania (Southern armyworm).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
OX NCBI_TaxID=6759, 7130, 7067, 37547;
RN [1]
RP SEQUENCE.
RC SPECIES=C. maenas; TISSUE=pericardial organs;
RA Stangler J., Hilbich C., Beyreuther K., Keller R.;
RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
shore crab Carcinus maenas.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579(1987).
RN [2]
RP SEQUENCE.
RC SPECIES=M. sexta;
RX MEDLINE=93050243; PubMed=1426284;
RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tumbiltz N.J.;
RT "Primary structure of a cardioactive neuropeptide from the tobacco
hawkmoth, Manduca sexta.";
RL FEBS Lett. 313:165-168(1992).
RN [3]
RP SEQUENCE.
RC SPECIES=T. molitor, and S. eridania; TISSUE=Head;
RX MEDLINE=94176032; PubMed=8129851;
RA Fuyuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
Schooley D.A.;
RT "Isolation and identification of a cardioactive peptide from Tenebrio
molitor and Spodoptera eridania.";
RL Biol. Chem. Hoppe-Seyler 374:1065-1074(1993).
CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHRONOTROPIC.
CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
INTO THE HEMOLYMPH.
DR PIR: A26363; A26363.
DR PIR: S27233; S27233.
KW Neuropeptide; Amidation.
FT DISULFID 3 9
FT MOD_RES 9 9 AMIDATION.
SEQUENCE 9 AA: 959 MW: C5A861A9CDD44EB9 CRC64;
Query Match 32.8%; Score 20; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 TGC 12
Db 7 TGC 9
RESULT 4
CONO_CONST STANDARD; PRT: 9 AA.
ID CONO_CONST
AC P05487;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
DE Arg-conopressin S.
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
Gray W.R., Oliveira B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
peptides from Conus geographus and Conus striatus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Oliveira B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

DR PIR: A28495; B28495.
 DR InterPro: IPR000981; Neurohypophys_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KM Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1031 MW; 17EB176B84540050 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRG 4
 III
 DB 7 PRG 9

RESULT 5
 OXYT_CYPCA STANDARD; PRT; 9 AA.
 ID OXYT_CYPCA
 DT P23879; 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Vasotocin.
 OS Cyprinus carpio (Common carp), and
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
 OC Cypriniformes; Cyprinidae; Cyprinus.
 OX NCBI_TaxId=7962; 7757;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C. carpio; TISSUE=pituitary;
 RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
 RT "Characterization of neurohypophyseal hormones from a fresh water bony
 RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
 RT water bony fishes.";
 RL Comp. Biochem. Physiol. 14:245-254(1965).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P. marinus; TISSUE=pituitary;
 RA MEDLINE=88225976; PubMed=3371648;
 RX Lane T.F., Sower S.A., Kawachi H.;
 RT "Arginine vasotocin from the pituitary gland of the lamprey
 RT (Petromyzon marinus): isolation and amino acid sequence.";
 RL Gen. Comp. Endocrinol. 70:152-157(1988).
 CC -1- FUNCTION: ANTIDIURETIC HORMONE.
 CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 PIR: B61364; B61364.
 PIR: S06375; S06375.
 DR InterPro: IPR000981; Neurohypophys_horm.
 DR Pfam: PF00220; hormone4; 1.
 DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
 KM Hormone; Amidation.
 FT DISULFID 1 6
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA; 1053 MW; 17EB176B8456D04B CRC64;

Query Match 29.5%; Score 18; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRG 4
 III
 DB 7 PRG 9

RESULT 6
 NUHM_CANPA

ID NUHM_CANPA STANDARD; PRT; 11 AA.
 AC P49820;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Fragment).
 GN NDUFY2.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE.

RC TISSUE=heart;
 RX MEDLINE=9816340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
 CC FRAGMENT OF THE ENZYME.
 CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -1- COFACTOR: 2FE-2S IRON-SULFUR CLUSTER N 1B.
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
 CC THIS IS A COMPONENT OF THE FLAVOPROTEIN FRACTION.
 CC -1- SUBCELLULAR LOCATION: MATRIX AND CYTOPLASMIC SIDE OF THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 24 kDa SUBUNIT FAMILY.
 DR HSC-2DPAGE; P49820; DOG.
 DR InterPro: IPR002023; Complex1_24kd.
 DR PROSITE: PS01099; COMPLEX1_24K; PARTIAL.
 DR Oxidoreductase; NAD; ubiquinone; Mitochondrion; Iron-sulfur.
 KM NON TER 11 11
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1099 MW; 267F5369C72DD8 CRC64;

Query Match 29.5%; Score 18; DB 1; Length 11;
 Best Local Similarity 50.0%; Pred. NO. 2.7e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 GGSVLV 9,
 III:
 DB 3 GGALFV 8

RESULT 7
 THYF_PIG STANDARD; PRT; 9 AA.
 ID THYF_PIG
 AC P01255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxId=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78026571; PubMed=914862;
 RA Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
 RT "Structural study of circulating thymic factor: a peptide isolated
 RT from pig serum. II. Amino acid sequence.";
 RL J. Biol. Chem. 252:8045-8047(1977).
 CC -1- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
 CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
 DR PIR: A01523; YFPG.
 FT MOD_RES 1 1
 SQ SEQUENCE 9 AA; 876 MW; D500B87866C5B3D CRC64;

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Query Match          27.9%; Score 17; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGS 6
   |||
Db 5 QGS 8

RESULT 8
VIAK_MSSV STANDARD; PRT; 12 AA.
ID VIAK_MSSV
AC P82006;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
   14.5 kDa structural polyprotein (Fragment).
   White spot syndrome virus (WSSV).
   Viruses; Unassigned viruses.
OC Viruses; Unassigned viruses.
OX NCBI_TaxID=92652;
RN [1]
RP SEQUENCE.
RC STRAIN=South Carolina;
RX MEDLINE=2021421; PubMed=10752552;
RT Wang Q., Poulos B.T., Lightner D.V.;
RT "Protein analysis of geographic isolates of shrimp white spot syndrome
   virus.";
RL Arch. Virol. 145:263-274(2000).
CC -!- FUNCTION: STRUCTURAL COMPONENT OF THE VIRION.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1242 MW; 248BDE4FDD21A338 CRC64;

Query Match          27.9%; Score 17; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RGS 5
   |||
Db 3 RGS 5

RESULT 9
RS7_MYCIT STANDARD; PRT; 8 AA.
ID RS7_MYCIT
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
   Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: PROTEIN S7 BINDS SPECIFICALLY TO PART OF THE 3' END OF
   16S RIBOSOMAL RNA (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: L08171; AAA25376.1; -.
DR PIR: S35538; S35538.
DR InterPro: IPR000235; Ribosomal_S7.
DR PROSITE: PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT INIT_MET 0
FT NON_TER 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match          26.2%; Score 16; DB 1; Length 8;
Best Local Similarity 75.0%; Pred. No. 1e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRG 5
   |||
Db 1 PRG 4

RESULT 10
TKNA_SCYCA STANDARD; PRT; 11 AA.
ID TKNA_SCYCA
AC P4133;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Substance P.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeidae; Carcharhiniformes;
OX Scyliorhinidae; Scyliorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=93292508; PubMed=7685693;
RA Waugh D., Wang Y., Hazen N., Balmert R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
   peptides from the brain of the dogfish, scyliorhinus canicula.";
RL Eur. J. Biochem. 214:469-474(1993).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
   EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
   SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
   MUSCLES.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC PIR: S33300; S33300.
DR InterPro: IPR003580; Protachykinin.
DR InterPro: IPR002040; Tachykinin.
DR Pfam: PF02202; Tachykinin; 1.
DR SMART: SM00203; TK; 1.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation; Neurotransmitter.
FT MOD_RES 11
SQ SEQUENCE 11 AA; 1278 MW; 214860DEC9D60867 CRC64;

Query Match          26.2%; Score 16; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PRG 5
   |||
Db 2 PRG 5

RESULT 11
CONO_CONGE STANDARD; PRT; 9 AA.
ID CONO_CONGE
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
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DT 01-Met-1995 (Rel. 32, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OX Neogastropoda; Conoidea; Conidae; Conus.
RN NCB1_TaxID=6491;
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramillo C.A., Zeikus R.D.,
RT Gray W.R., Olivera B.M.;
RT "Invertebrate Vasopressin/oxytocin homologs. Characterization of
peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 263:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR PIR; A28495; A28495.
RN InterPro: IPR000981; Neurohypophys_horm.
RFam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KM Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRG 4
   1 1
Db 7 PKG 9

RESULT 12
MGMT_BOVIN
ID MGMT_BOVIN STANDARD: PRT: 9 AA.
AC P29177;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63) (6-O-
methylguanine-DNA methyltransferase) (Fragment).
GN MGMT.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
RN NCB1_TaxID=9913;
RP [1]
RP TISSUE=Thymus;
RX MEDLINE=90174912; PubMed=2308822;
RA Rydberg B., Hall J., Karan P.;
RT "Active site amino acid sequence of the bovine 6-methylguanine-DNA
methyltransferase.";
RL Nucleic Acids Res. 18:17-21(1990).
CC -1- FUNCTION: REPAIR OF ALKYLATED GUANINE IN DNA BY STOICHIOMETRICALLY
TRANSFERRING THE ALKYL GROUP AT THE O-6 POSITION TO A CYSTEINE
RESIDUE IN THE ENZYME. THIS IS A SUICIDE REACTION: THE ENZYME IS
IRREVERSIBLY INACTIVATED.
CC -1- CATALYTIC ACTIVITY: DNA (containing 6-O-methylguanine) +
[protein]-L-cysteine -> DNA (without 6-O-methylguanine) +
protein
S-methyl-L-cysteine.
CC -1- SIMILARITY: WITH SEGMENTS OF E. COLI ADA AND OCT METHYLTRANSFERASE
WHICH ENCOMPASS THE ALKYL-ACCEPTOR RESIDUES.
DR InterPro: IPR001497; Methyltransf_1.

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DR PROSITE: PS00374; MGMT; PARTIAL.
KM DNA repair; Transferase; Methyltransferase.
FT NON_TER 1 1
FT ACT_SITE 9 9 ALKYL GROUP ACCEPTOR (BY SIMILARITY).
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 967 MW; 325171A720476047 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 8 LVTCG 12
   :| |
Db 5 ILTPC 9

RESULT 13
BRK_ONCMY
ID BRK_ONCMY STANDARD: PRT: 10 AA.
AC 09PR21;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCB1_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE=94039817; PubMed=8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
trout plasma.";
RL FEBS Lett. 334:75-78(1993).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -1- SUBCELLULAR LOCATION: secreted.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KM Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 24.6%; Score 15; DB 1; Length 10;
Best Local Similarity 57.1%; Pred. No. 7.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 PRGSVL 8
   | | | |
Db 3 PGWSPSL 9

RESULT 14
CXAL_CONIM
ID CXAL_CONIM STANDARD: PRT: 12 AA.
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alpha-conotoxin ImI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCB1_TaxID=35631;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RP TISSUE=Venom;
RX MEDLINE=94266889; PubMed=8206995;
RA McIntosh J.M., Yoshikami D., Mahe E., Nielsen D.B., Rivier J.E.,
Gray W.R., Olivera B.M.;

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RT "A nicotinic acetylcholine receptor ligand of unique specificity,
RT alpha-conotoxin ImI."
RL J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=95379776; PubMed=7651351;
RA Johnson D.S., Martinez J., Elgoyhen A.B., Heinemann S.F.,
RA McIntosh J.M.;
RT "Alpha-conotoxin ImI exhibits subtype-specific nicotinic
RT acetylcholine receptor blockade: preferential inhibition of homomeric
RT alpha 7 and alpha 9 receptors."
RL Mol. Pharmacol. 48:194-199(1995).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=99212205; PubMed=10194298;
RA Rogers J.P., Lugibuhl P., Shen G.S., McCabe R.T., Stevens R.C.,
RA Weimer D.E.;
RT "NMR solution structure of alpha-conotoxin ImI and comparison to
RT other conotoxins specific for neuronal nicotinic acetylcholine
RT receptors."
RL Biochemistry 38:3874-3882(1999).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=99158061; PubMed=10050774;
RA Maslennikov I.V., Shengkarev Z.O., Zhmak M.N., Ivanov V.T.,
RA Methfessel C., Tsetlin V.I., Arseniev A.S.;
RT "NMR spatial structure of alpha-conotoxin ImI reveals a common
RT scaffold in small and snake toxins recognizing neuronal nicotinic
RT acetylcholine receptors."
RL FEBS Lett. 444:275-280(1999).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE=99324017; PubMed=10395477;
RA Gehrmann J., Daly N.L., Alewood P.F., Craik D.J.;
RT "Solution structure of alpha-conotoxin ImI by 1H nuclear magnetic
RT resonance."
RL J. Med. Chem. 42:2364-2372(1999).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
CC RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
CC WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGETS NEURONAL
CC NACHRS IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
CC WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
CC WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
CC ALPHA-2/BETA-2, ALPHA-3/BETA-2, ALPHA-4/BETA-2, ALPHA-2/BETA-4,
CC ALPHA-3/BETA-4, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE ALPHA-TYPE CONOTOXIN FAMILY.
DR PDB: 1IM1; 15-JUN-99.
DR PDB: 1IM1; 23-APR-99.
DR PDB: 1CNL; 27-MAY-99.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom; 3D-structure.
FT DISULFID 2 8
FT DISULFID 3 12
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1357 MW; 9C29CEA545A4176A CRC64;

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Query Match 24.6%; Score 15; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. NO. 9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glutitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalae; Hypnosqualae; Pristigasterae; Batoidae;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurophyophyseal peptides: isolation of a new hormone,
RT glutitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
RT the ray (Raja clavata)."
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -1- FUNCTION: ANTIIDURETIC HORMONE.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurophopsys_horm.
DR Pfam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

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Query Match 23.0%; Score 14; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. NO. 1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PG 4
DB 7 PG 9

Search completed: October 10, 2002, 06:21:20
Job time: 356 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:23:38 ; Search time 43.8 Seconds
(without alignments)
47.396 Million cell updates/sec

Title: US-09-629-719D-8
Perfect score: 61
Sequence: 1 XPRGGSVLTGTC 12

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 1842

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp_invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	45.9	11	7	077876
2	24	39.3	11	13	09PS22
3	21	34.4	10	4	0960A7
4	21	34.4	11	4	075811
5	21	34.4	12	4	013865
6	21	34.4	12	4	096P98
7	19	31.1	10	4	09H115
8	19	31.1	10	4	09P229
9	18	29.5	7	11	063480
10	18	29.5	8	2	09R4M3
11	18	29.5	10	13	090Y93
12	18	29.5	11	12	0997C1
13	18	29.5	12	2	002128
14	18	29.5	12	5	017140
15	18	29.5	12	8	09G196
16	18	29.5	12	10	041856

17	17	27.9	8	4	096RN9	096rn9 homo sapien
18	17	27.9	9	2	099193	099193 pseudomonas
19	17	27.9	10	2	052837	052837 rhizobium 1
20	17	27.9	11	4	090CP5	090cp5 homo sapien
21	17	27.9	11	7	077892	077892 oreochromis
22	17	27.9	11	7	077893	077893 oreochromis
23	17	27.9	11	7	077906	077906 oreochromis
24	17	27.9	11	11	090XM6	090xm6 mus musculu
25	17	27.9	12	2	046712	046712 escherichia
26	17	27.9	12	6	046664	046664 macropus ro
27	17	27.9	12	10	093X21	093x21 zea mays (m
28	16	26.2	8	12	09E807	09e807 beet soil-b
29	16	26.2	8	12	09E805	09e805 beet soil-b
30	16	26.2	8	12	09DSN6	09dsn6 beet soil-b
31	16	26.2	8	12	09E805	09e805 beet soil-b
32	16	26.2	8	12	09E803	09e803 beet soil-b
33	16	26.2	8	12	09DSN4	09dsn4 beet soil-b
34	16	26.2	8	12	09DSN2	09dsn2 beet soil-b
35	16	26.2	8	12	09DSN2	09dsn2 beet soil-b
36	16	26.2	8	12	09E802	09e802 beet soil-b
37	16	26.2	8	12	09E801	09e801 beet soil-b
38	16	26.2	8	12	09DSN1	09dsn1 beet soil-b
39	16	26.2	8	12	09DSN0	09dsn0 beet soil-b
40	16	26.2	8	12	09E800	09e800 beet soil-b
41	16	26.2	8	12	09E8P9	09e8p9 beet soil-b
42	16	26.2	8	12	09E8P8	09e8p8 beet soil-b
43	16	26.2	8	12	09E8P7	09e8p7 beet soil-b
44	16	26.2	10	4	014096	014096 homo sapien
45	16	26.2	11	2	047451	047451 escherichia

ALIGNMENTS

RESULT	1	ALIGNMENTS
ID	077876	PRELIMINARY; PRT; 11 AA.
AC	077876;	
DT	01-NOV-1998 (TREMBLrel. 08, Created)	
DT	01-NOV-1998 (TREMBLrel. 08, last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, last annotation update)	
DE	MHC CLASS II B LOCUS 1 (FRAGMENT).	
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;	
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidel;	
OC	Cichlidae; Oreochromis.	
OX	NCBI_TaxID=8128;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=98315113; PubMed=9649539;	
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,	
RA	Ligueroa F., Sultmann H., Klein J.;	
RT	"Linkage relationships and haplotype polymorphism among cichlid mhc	
RT	class II B loci."	
RL	Genetics 149:1527-1537(1998).	
DR	EMBL; AF049985; AAC41324.1; -.	
FT	NON_TER 1	
FT	NON_TER 11	
SO	SEQUENCE 11 AA; 1178 MW; 9AC131FAB2D2DB45 CRC64;	

Query Match 45.9%; Score 28; DB 7; Length 11;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 SYLVYTC 12
DB 4 SYVYTC 10
RESULT 2

ID Q9PS22 PRELIMINARY; PRT; 11 AA.
AC Q9PS22;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE HYDRIN 1', VASOTOCINYL-GLY-LYS.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE.
RX MEDLINE=93200145; PubMed=8452872;
RA Iwamuro S., Hayashi H., Kikuyama S.;
RT "An additional arginine-vasotocin-related peptide, vasotocinyl-Gly-Lys, in Xenopus neurohypophysis.";
RT Biochim. Biophys. Acta 1176:143-147(1993).
RT InterPro: IPR000981; Neurohypophys_horm.
FTam: PF00220; hormone4; 1.
DR PROSITE: PS00264; NEUROHYPOPHYS_HORM; 1.
SQ SEQUENCE 11 AA; 1238 MW; CCSB57EB176EB456 CRC64;

Query Match 39.3%; Score 24; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGS 5
ID 1111
DB 7 PRGS 10

RESULT 3
Q960A7 PRELIMINARY; PRT; 10 AA.
AC Q960A7;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE BA151A2.1 (CDC42 GUANINE EXCHANGE FACTOR (GEF) 9 (COLLYBISTRIN, PEM-2, HPEM-2, KIAA0424)) (FRAGMENT).
DE HPEM-2, KIAA0424)) (FRAGMENT).
GN ARHGAP9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RA Whitehead S.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL451106; CAC88408.1; -;
FT NON_TER 10
SQ SEQUENCE 10 AA; 1122 MW; 39925C8B78640043 CRC64;

Query Match 34.4%; Score 21; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RGGS 6
ID 1111
DB 5 RGGS 8

RESULT 4
Q75811 PRELIMINARY; PRT; 11 AA.
ID 075811
AC 075811;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ERBB-3 R2 (FRAGMENT).

GN C-ERBB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARIAN CARCINOMA;
RX MEDLINE=98345147; PubMed=9681822;
RA Lee H., Mainle N.J.;
RT "Isolation and characterization of four alternate c-erbB3 transcripts expressed in ovarian carcinoma-derived cell lines and normal human tissues.";
RT Lissues";
RT Oncogene 16:3243-3252(1998).
RL EMBL; U88358; AAC39858.1; -;
FT NON_TER 1
SQ SEQUENCE 11 AA; 1017 MW; 21B23636EB72878 CRC64;

Query Match 34.4%; Score 21; DB 4; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGS 5
ID 1111
DB 8 PRGS 11

RESULT 5
Q13865 PRELIMINARY; PRT; 12 AA.
AC Q13865;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KINESIN LIGHT CHAIN.
GN BETA-KINESIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=97101110; PubMed=8945637;
RA Chernajovsky Y., Brown A., Jones T.A.;
RT "Promoter first exon/intron characterization and chromosomal location of the human light chain (beta) kinesin gene.";
RL DNA Cell Biol. 15:965-974(1996).
DR EMBL; X69658; CAA49349.1; -;
SQ SEQUENCE 12 AA; 1274 MW; 3FB8D34EE165A5B8 CRC64;

Query Match 34.4%; Score 21; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 RGGS 6
ID 1111
DB 3 RGGS 6

RESULT 6
Q96P98 PRELIMINARY; PRT; 12 AA.
ID Q96P98
AC Q96P98;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CD27-BINDING PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kang H.S., Park Y.J., Jung H.M., Jun D.Y., Huh T.L., Kim Y.H.;
 RT "Characterization of TPA-responsive genes in U937 cells using ordered
 RT differential display PCR."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401214; AAL02171.1; -
 FT NON_TER
 SO SEQUENCE 12 AA; 1333 MW; 977A27103ADEA5A1 CRC64;

Query Match
 Best Local Similarity 34.4%; Score 21; DB 4; Length 12;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 7 VLVTGC 12
 DB 2 VLCTSC 7

RESULT 7
 ID 09H115 PRELIMINARY; PRT; 10 AA.
 AC 09H115;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE MUTANT BETA-GLOBIN (FRAGMENT).
 GN HBB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yang Z., Chu J., Ban G., Shi L., Huang X., Lin K., Tao Y.;
 RT "Molecular characterization of beta thalassemia in Yunnan, China."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY013300; AAG46183.1; -
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 10 AA; 1042 MW; 2210B2A2C732C448 CRC64;

Query Match
 Best Local Similarity 31.1%; Score 19; DB 4; Length 10;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 GSVLV 9
 DB 3 GNVLV 7

RESULT 8
 ID 09P229 PRELIMINARY; PRT; 10 AA.
 AC 09P229;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE EPIDERMAL GROWTH FACTOR RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91337091; PubMed=1678600;
 RA Humphrey P.A., Gangarosa L.M., Wong A.J., Archer G.E.,
 RA Lund-Johansen M., Bjerkvig R., Laetum O.D., Friedman H.S.,
 RA Bigner D.D.;
 RT "Deletion-mutant epidermal growth factor receptor in human gliomas;

RT effects of type II mutation on receptor function."
 RL Biochem. Biophys. Res. Commun. 178:1413-1420(1991).
 DR EMBL; S51343; AAB19486.2; -
 KW Receptor.
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 10 AA; 1020 MW; 439DEFE8B87B1727 CRC64;

Query Match
 Best Local Similarity 31.1%; Score 19; DB 4; Length 10;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 LVYGC 12
 DB 3 LVGCG 7

RESULT 9
 ID 063480 PRELIMINARY; PRT; 7 AA.
 AC 063480;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TR4-NS ORPHAN RECEPTOR (FRAGMENT).
 GN TR4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96198747; PubMed=8612486;
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
 RA Detera-Madliegh S.D.;
 RT "Splice variants of rat TR4 orphan receptor: differential expression
 RT of novel sequences in the 5'-untranslated region and C-terminal
 domain."
 RL Endocrinology 137:1562-1571(1996).
 DR EMBL; U59125; AAB02827.1; -
 KW Receptor.
 FT NON_TER
 FT NON_TER
 SO SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match
 Best Local Similarity 29.5%; Score 18; DB 11; Length 7;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 RGGSV 7
 DB 3 RGGDL 7

RESULT 10
 ID 09R4M3 PRELIMINARY; PRT; 8 AA.
 AC 09R4M3;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE COBI-BACTERIAL SEX PHEROMONE.
 OS Enterococcus faecalis (Streptococcus faecalis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
 OC Enterococcus.
 OX NCBI_TaxID=1351;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95290767; PubMed=7772836;
 RA Nakayama J., Abe Y., Ono Y., Isogai A., Suzuki A.;
 RT "Isolation and structure of the Enterococcus faecalis sex pheromone,
 RT COBI, that induces conjugal transfer of the hemolysin/bacteriocin

RT plasmids, POB1 and pY11."
 RL Biosci. Biotechnol. Biochem. 59:703-705(1995).
 SO SEQUENCE 8 AA: 741 MW: 83D87732C732CDC2 CRC64;

Query Match 29.5%; Score 18; DB 2; Length 8;
 Best Local Similarity 66.7%; Pred. No. 5.6e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 SVLVGT 11
 :|||
 Db 2 AVLVG 7

RESULT 11
 ID 090Y93 PRELIMINARY; PRT; 10 AA.
 090Y93: 01-DEC-2001 (TREMBlrel. 19, Created)
 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE GROWTH HORMONE (FRAGMENT).
 GN GH.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KENASKU N., NAKADA A., YAGI E., OKABAYASHI H., GUEMENE D.;
 RT "Genetic variation of chicken growth hormone gene."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB061722; BAB69037.1; -
 FT NON_TER 1 1
 FT NON_TER 10 10
 SO SEQUENCE 10 AA: 1155 MW: 684175175A40AAB CRC64;

Query Match 29.5%; Score 18; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRG 4
 :||
 Db 7 PRG 9

RESULT 12
 ID 0997C1 PRELIMINARY; PRT; 11 AA.
 AC 0997C1: 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE COAT PROTEIN (FRAGMENT).
 OS East African cassava mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=62079;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=21103006; PubMed=11172108;
 RA Pita J.S., Fondong V.N., Sangare A., Otim-Nape G.W., Ogwal S.,
 RA Fauguet C.M.;
 RT "Recombination, pseudorecombination and synergism of geminiviruses are
 RT determinant keys to the epidemic of severe cassava mosaic disease in
 RT Uganda."
 RT J. Gen. Virol. 82:655-665(2001).
 DR EMBL; AF230374; AAK26738.1; -
 FT NON_TER 11 11
 SO SEQUENCE 11 AA: 1216 MW: 7751D0695AA86774 CRC64;

Query Match 29.5%; Score 18; DB 12; Length 11;
 Best Local Similarity 25.0%; Pred. No. 1e+04;
 Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 3 RGSVLVT 10
 | :|||
 Db 4 RPDIIIS 11

RESULT 13
 ID 002128 PRELIMINARY; PRT; 12 AA.
 AC 002128: 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN HYDA 5' REGION (FRAGMENT).
 OS Desulfovibrio vulgaris (strain Hildenborough)
 OC Bacteria; Proteobacteria; delta subdivision; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9307640; PubMed=7686524;
 RA Van den Berg W.A.M., Stokermans J.P.W.G., Van Dongen W.M.A.M.;
 RT "The operon for the Fe-hydrogenase in Desulfovibrio vulgaris
 RT (Hildenborough): mapping of the transcript and regulation of
 RT expression."
 RL FEWS Microbiol. Lett. 110:85-90(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85203856; PubMed=3888621;
 RA Voordouw G., Brenner S.;
 RT "Nucleotide sequence of the gene encoding the hydrogenase from
 RT Desulfovibrio vulgaris (Hildenborough)."
 RL Eur. J. Biochem. 148:515-520(1985).
 RN [3]
 RP REVISIONS.
 RA Van den Berg W.A.M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z15142; CAB37617.1; -
 KW Hypothetical protein.
 FT NON_TER 1 1
 SO SEQUENCE 12 AA: 1261 MW: C831123540BAA9CD CRC64;

Query Match 29.5%; Score 18; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRG 4
 :||
 Db 10 PRG 12

RESULT 14
 ID 017140 PRELIMINARY; PRT; 12 AA.
 AC 017140: 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JAN-1998 (TREMBlrel. 05, Last annotation update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE PUTATIVE C-MYC HOMOLOG (FRAGMENT).
 OS Crassostrea virginica (Eastern oyster).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
 OC Ostreoidae; Ostreidae; Crassostrea.
 OX NCBI_TaxID=6565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=WESTERN NORTH ATLANTIC WILD OYSTER;
 RA Hare M.P., Avise J.C.;
 RT "Population structure in the American Oyster as inferred by Nuclear
 RT Gene Genealogies."
 RL Mol. Biol. Evol. 0:0-0(1997).

DR EMBL: AF024522; AAB82269.1; -.
 FT NON_TER 1 1
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1334 MW; FF6312ABFE1775AA CRC64;

Query Match 29.5%; Score 18; DB 5; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 PRG 4
 Db 7 PRG 9

RESULT 15
 O9G196 PRELIMINARY; PRT; 12 AA.
 ID O9G196;
 AC O9G196;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 RIBULOSE-1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE SMALL SUBUNIT
 (FRAGMENT).
 DE RBCS.
 GN Sargassum polycystum.
 OS Chloroplast.
 OG Eukaryota; stramenopiles; Phaeophyceae; Fucales; Sargassaceae;
 OC Sargassum.
 OX NCBI_TaxId=127578;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEP127;
 RA Phillips N.E.;
 RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
 (Fucales, Phaeophyceae).";
 RL Thesis (1998), University of Hawaii.
 RN 12
 RP SEQUENCE FROM N.A.
 RC STRAIN=NEP127;
 RA Phillips N.E., Smith C.M., Morden C.W.;
 RT "Testing the systematics of the genus Sargassum (Fucales,
 Phaeophyceae) with the Rubisco operon.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF244344; AAF98114.1; -.
 KW Chloroplast.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1379 MW; 373D121250CEB867 CRC64;

Query Match 29.5%; Score 18; DB 8; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 8 LVTGC 12
 Db 3 LTPGC 7

Search completed: October 10, 2002, 06:23:38
 Job time: 389 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:16:24 ; Search time 47.09 Seconds
(without alignments)
28.305 Million cell updates/sec

Title: US-09-629-719D-8
Perfect score: 61
Sequence: 1 XPRGGSVLYTGC 12

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 158732

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A.GeneSeq.032802:*

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- 21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	83.6	11	16	ICAM CD54 (38-48)
2	45	73.8	12	16	ICAM CD54 (37-48)
3	45	73.8	12	16	ICAM CD54 (37-48)
4	45	73.8	12	16	ICAM CD54 (37-48)
5	45	73.8	12	18	ICAM-1 beta subunit
6	40	49.2	11	20	ICAM-1 beta subunit
7	38	45.9	5	10	Human thioredoxin
8	28	45.9	5	19	Sequence of part o
9	28	45.9	6	14	ICAM-1 peptide fra
10	28	45.9	6	14	Peptide which bind
11	28	45.9	7	18	PKB substrate #26.

12	28	45.9	7	21	AAV63234	Protocadherin cell
13	28	45.9	8	21	AAV63237	Protocadherin cell
14	28	45.9	9	21	AAV63240	Protocadherin cell
15	28	45.9	10	21	AAV63243	Protocadherin cell
16	28	45.9	10	22	AAV696703	Human complementar
17	28	45.9	10	22	AAV696811	Human complementar
18	28	45.9	10	22	AAV696815	Human complementar
19	28	45.9	11	21	AAV63246	Protocadherin cell
20	27	44.3	6	14	AAV63246	Antigen to generat
21	27	44.3	6	14	AAV63246	Antigen to generat
22	27	44.3	6	14	AAV63246	Antigen to generat
23	27	44.3	6	14	AAV63246	Antigen to generat
24	27	44.3	12	21	AAV54514	Molecular mimetic
25	27	44.3	12	21	AAV54514	Human CD4 protein
26	26	42.6	9	14	AAV31421	Cyclic cell adhesi
27	26	42.6	9	21	AAV31421	Cyclic platelet ag
28	26	42.6	10	21	AAV87210	Hepatitis GB virus
29	26	42.6	10	22	AAV87210	Human secreted pro
30	26	42.6	10	22	AAV87210	Human gene 58 enco
31	26	42.6	10	22	AAV87210	Saccharomyces cere
32	26	42.6	10	22	AAV87210	Saccharomyces cere
33	25	41.0	9	19	AAV20162	Human presentin I
34	25	41.0	10	16	AAV74919	urea plasmidogen a
35	25	41.0	10	20	AAV06180	scfv 9A4 clone 4H
36	25	41.0	10	21	AAV03166	Plasmid PBS24ubenv
37	25	41.0	10	22	AAV50194	Monoclonal antibod
38	25	41.0	10	22	AAV50194	Saccharomyces cere
39	25	41.0	10	22	AAV72784	Antibacterial pept
40	25	41.0	10	22	AAV72785	Antibacterial pept
41	25	41.0	10	22	AAV57730	D. tetsisleri IDW pe
42	25	41.0	11	20	AAV42019	Rheumatoid arthrit
43	25	41.0	12	10	AAV91137	Partial sequence o
44	25	41.0	12	10	AAV91134	Partial sequence o
45	24	39.3	5	14	AAV34099	Peptide which bind

ALIGNMENTS

RESULT 1	
AAV80118	
ID	AAV80118 standard; Peptide; 11 AA.
AC	XX
DT	05-MAR-1996 (first entry)
XX	XX
DE	ICAM CD54 (38-48) peptide MC-1-80.
XX	XX
KW	ICAM-1; CD54; intercellular adhesion molecule-1; Integrin; LFA-1;
KW	Leucocyte function-associated antigen; Immunosuppressive;
OS	MC-1-80.
XX	XX
OS	Synthetic.
FT	Key
FT	Misc-difference 11
FT	Location/Qualifiers
FT	/note= "Cys at position 48 of CD54 is Gly
FT	at position 11 of MC-1-80"
PN	MO9528170-A1.
PD	26-OCT-1995.
XX	XX
PF	19-APR-1995; 95WO-US04886.
XX	XX
PR	19-APR-1994; 94US-0229513.
XX	XX
PA	(UNITV) UNITV KANSAS.
XX	XX
PI	Benedict S, Chan MA, Siahaan TJ, Tibbetts SA;
XX	XX
DR	WPI; 1995-373631/48.

XX Changing peptide reactivity via conjugation with a second peptide
 PT causes change in conformation of first peptide, pref. LFA-1 and
 CC ICAM-1 functional domain derived peptide(s)
 XX
 PS Claim 30; Page 42; 64pp; English.
 CC
 CC Synthetic sub-sequences of ICAM-1 CD54 (AAR80113-24), LFA-1 beta CD18
 CC (AAR80109) or LFA-1 alpha CD11a (AAR80111-12) are used to block
 CC ICAM/LFA binding interaction by binding to a target protein in a
 CC manner that precludes the normal binding reaction between ICAM-1 and
 CC LFA-1. Alternatively, the peptide induces a conformational change
 CC in the target protein, enhancing the reactivity of a second
 CC peptide. The peptides have immunosuppressive appln.
 CC
 SO Sequence 11 AA;

Query Match 83.6%; Score 51; DB 16; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.052;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGGSVLVTG 11
 DB 2 prggsvlvtg 11

RESULT 2
 AAR80117
 ID AAR80117 standard; Peptide; 12 AA.
 AC AAR80117;
 XX
 XX
 DT 05-MAR-1996 (first entry)
 XX

DE ICAM CD54 (37-48) cyclic peptide RB-1-51.
 XX
 XX ICAM-1; CD54; intercellular adhesion molecule-1; Integrin; LFA-1;
 KW leucocyte function-associated antigen; immunosuppressive;
 XX RB-1-51; cyclic.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "Ile at position 37 of CD54 is Cys
 FT at position 1 of RB-1-51"
 FT Disulfide-bond 1..12
 XX /note= "cysteine-cysteine disulfide bond"
 PN WO9528170-A1.

XX 26-OCT-1995.
 PD
 XX 19-APR-1995; 95WO-US04886.
 PF
 XX 19-APR-1994; 94US-0229513.
 PR
 XX (UNITV) UNITV KANSAS.
 PA
 XX

PI Benedict S, Chan MA, Siahaan TJ, Tibbetts SA;
 XX
 XX WPI: 1995-373631/48.
 DR
 XX Changing peptide reactivity via conjugation with a second peptide
 PT causes change in conformation of first peptide, pref. LFA-1 and
 CC ICAM-1 functional domain derived peptide(s)
 CC
 PS Claim 30; Page 42; 64pp; English.

CC Synthetic sub-sequences of ICAM-1 CD54 (AAR80113-24), LFA-1 beta CD18
 CC (AAR80109) or LFA-1 alpha CD11a (AAR80111-12) are used to block
 CC ICAM/LFA binding interaction by binding to a target protein in a

CC manner that precludes the normal binding reaction between ICAM-1 and
 CC LFA-1. Alternatively, the peptide induces a conformational change
 CC in the target protein, enhancing the reactivity of a second
 CC peptide. The peptides have immunosuppressive appln.
 CC
 SO Sequence 12 AA;

Query Match 73.8%; Score 45; DB 16; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGGSVLVT 10
 DB 3 prggsvlvt 11

RESULT 3
 AAR80116
 ID AAR80116 standard; Peptide; 12 AA.
 AC AAR80116;
 XX
 XX
 DT 05-MAR-1996 (first entry)
 XX

DE ICAM CD54 (37-48) peptide SC-3-150.
 XX
 XX ICAM-1; CD54; intercellular adhesion molecule-1; Integrin; LFA-1;
 KW leucocyte function-associated antigen; immunosuppressive;
 XX SC-3-150.
 OS Synthetic.

XX Key Location/Qualifiers
 FH Misc-difference 1 /note= "Ile at position 37 of CD54 is Cys
 FT at position 1 of SC-3-150"
 FT WO9528170-A1.
 PN

XX 26-OCT-1995.
 PD
 XX 19-APR-1995; 95WO-US04886.
 PF
 XX 19-APR-1994; 94US-0229513.
 PR
 XX (UNITV) UNITV KANSAS.
 PA

PI Benedict S, Chan MA, Siahaan TJ, Tibbetts SA;
 XX
 XX WPI: 1995-373631/48.
 DR
 XX Changing peptide reactivity via conjugation with a second peptide
 PT causes change in conformation of first peptide, pref. LFA-1 and
 CC ICAM-1 functional domain derived peptide(s)
 CC
 PS Claim 30; Page 41; 64pp; English.

CC Synthetic sub-sequences of ICAM-1 CD54 (AAR80113-24), LFA-1 beta CD18
 CC (AAR80109) or LFA-1 alpha CD11a (AAR80111-12) are used to block
 CC ICAM/LFA binding interaction by binding to a target protein in a
 CC manner that precludes the normal binding reaction between ICAM-1 and
 CC LFA-1. Alternatively, the peptide induces a conformational change
 CC in the target protein, enhancing the reactivity of a second
 CC peptide. The peptides have immunosuppressive appln.
 CC
 SO Sequence 12 AA;

Query Match 73.8%; Score 45; DB 16; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGGSVLVT 10
| | | | |
DB 3 prggsvlvt 11

RESULT 4
AAW34098
ID AAW34098 standard; peptide; 12 AA.

AC AAW34098;
XX
XX
DT 14-MAY-1998 (first entry)
XX
DE ICAM-1 beta subunit based peptide IB-R.
XX
XX ICAM-1; intracellular adhesion molecule-1; inhibitor; integrin binding;
KW lymphocyte fusion associated antigen-1; LFA-1; transplant rejection;
KW allergy; autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW insulin-dependent diabetes mellitus; therapy; beta subunit.
XX
OS Synthetic.
XX Homo sapiens.
XX WO9741149-A1.
XX
XX 06-NOV-1997.
XX
XX 24-APR-1997; 97WO-US06799.
XX
XX 23-APR-1997; 97US-0844978.
PR 26-APR-1996; 96US-0638437.
PR 26-APR-1996; 96US-0844978.
XX
XX (UNITV) UNITV KANSAS.
XX PA
XX Benedict S, Chan MA, Slihaan TJ, Tibbetts SA;
XX
XX WPI: 1997-549680/50.
XX
XX Composition of peptide(s) that inhibit binding between proteins -
PT used for treatment of transplant rejection, autoimmune disease and
PT allergy
XX
XX Claim 5; Page 18; 50pp; English.
XX
XX This sequence represents a peptide fragment of the beta subunit of
CC intracellular adhesion molecule-1 (ICAM-1). This sequence, or a fragment
CC of lymphocyte fusion associated antigen-1 (LFA-1), can be used in
CC the peptide composition (A) of the invention, which inhibits the binding
CC of first and second proteins (P1, P2) and comprises at least one peptide
CC that binds to P1 and at least one peptide that binds to P2. (A) is used,
CC in vivo or in vitro, to inhibit binding of integrins to their specific
CC binding proteins, particularly for treating transplant rejection, allergy
CC and autoimmune disease, specifically rheumatoid arthritis,
CC insulin-dependent diabetes mellitus and multiple sclerosis.
XX
XX Sequence 12 AA:
SQ

Query Match 73.8%; Score 45; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGGSVLVT 10
| | | | |
DB 3 prggsvlvt 11

RESULT 5
AAW34101
ID AAW34101 standard; peptide; 12 AA.
XX
XX AAW34101;
AC

XX
DT 14-MAY-1998 (first entry)
XX
XX ICAM-1 beta subunit based peptide cIB-C.
XX
XX ICAM-1; intracellular adhesion molecule-1; inhibitor; integrin binding;
KW lymphocyte fusion associated antigen-1; LFA-1; transplant rejection;
KW allergy; autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW insulin-dependent diabetes mellitus; therapy; beta subunit; cyclic.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..12
FT /note= "form disulphide bond to create cyclic peptide"
XX
XX WO9741149-A1.
XX
XX 06-NOV-1997.
XX
XX 24-APR-1997; 97WO-US06799.
XX
XX 23-APR-1997; 97US-0844978.
PR 26-APR-1996; 96US-0638437.
PR 26-APR-1996; 96US-0844978.
XX
XX (UNITV) UNITV KANSAS.
XX PA
XX Benedict S, Chan MA, Slihaan TJ, Tibbetts SA;
XX
XX WPI: 1997-549680/50.
XX
XX Composition of peptide(s) that inhibit binding between proteins -
PT used for treatment of transplant rejection, autoimmune disease and
PT allergy
XX
XX Claim 5; Page 19; 50pp; English.
XX
XX This sequence represents a cyclic peptide fragment of the beta subunit of
CC intracellular adhesion molecule-1 (ICAM-1). This sequence, or a fragment
CC of lymphocyte fusion associated antigen-1 (LFA-1), can be used in
CC the peptide composition (A) of the invention, which inhibits the binding
CC of first and second proteins (P1, P2) and comprises at least one peptide
CC that binds to P1 and at least one peptide that binds to P2. (A) is used,
CC in vivo or in vitro, to inhibit binding of integrins to their specific
CC binding proteins, particularly for treating transplant rejection, allergy
CC and autoimmune disease, specifically rheumatoid arthritis,
CC insulin-dependent diabetes mellitus and multiple sclerosis.
XX
XX Sequence 12 AA:
SQ

Query Match 73.8%; Score 45; DB 18; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.54;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGGSVLVT 10
| | | | |
DB 3 prggsvlvt 11

RESULT 6
AAW83406
ID AAW83406 standard; peptide; 11 AA.
XX
XX AAW83406;
AC
XX 23-FEB-1999 (first entry)
DT
DE Human thioredoxin reductase C-terminal peptide.
XX
XX Human; thioredoxin reductase; KM-102-derived reductase like factor;
KW

KW TR: KDRF: selenocysteine; arteriosclerosis; diabetes; oedema;
 KW Ischaemic lesion.
 OS Homo sapiens.
 XX JP10309193-A.
 PN
 XX 24-NOV-1998.
 PD
 XX
 PF 12-MAY-1997; 97JP-0120443.
 PR
 XX 12-MAY-1997; 97JP-0120443.
 XX
 PA (SANY) SANKYO CO LTD.
 XX
 DR WPI; 1999-063678/06.
 XX
 PT Preparation of a mammalian seleno-cysteine-containing protein in E.
 col1 - useful in the treatment of arteriosclerosis, diabetes,
 Ischaemic lesions and oedema
 PS Example; Page 12; 40pp; Japanese.
 XX
 CC The present sequence represents the C-terminal peptide from human
 CC thioredoxin reductase (TR). The TR protein is prepared by gene
 CC manipulation and has selenocysteine at position 503 of the mature
 CC amino acid sequence. The protein has thioredoxin reducing activity.
 CC The protein is useful as a preventive and treating agent for
 CC arteriosclerosis, diabetes, ischaemic lesions, oedema and many
 CC other diseases.
 CC
 SQ Sequence 11 AA:
 49.2%; Score 30; DB 20; Length 11;
 Query Match Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 4 GGSVLVTGC 12
 | | | | |
 Db 3 gasllqagc 11
 RESULT 7
 AAP80452
 ID AAP80452 standard; protein; 5 AA.
 XX AAP80452:
 28-DEC-1990 (first entry)
 DE Sequence of part of human intercellular adhesion molecule-1 (ICAM-1).
 XX
 KW Lymphocyte recognition; antiinflammatory agent;
 KW Lymphocyte function associated antigen 1 (LFA-1).
 XX
 OS Homo sapiens.
 XX
 PN AU8815518-A.
 PD
 XX 10-NOV-1988.
 PD
 XX 29-APR-1988; 88AU-0106901.
 PF
 XX 04-MAY-1987; 87US-0045963.
 PR 01-NOV-1987; 87US-0115798.
 PR 16-FEB-1988; 88US-0155954.
 XX
 PA (DANA-) DANA FARBER CANCER.
 XX
 PI Springer TA, Rothlein R, Marlin SD, Dustin ML.
 XX
 DR WPI; 1989-033081/05.

XX New inter-cellular adhesion molecule-7, derived antibodies etc. -
 PT are used for diagnosis and treatment of inflammation and
 PT tumours, and for new DNA coding sequences
 XX
 PS Claim 3(1); Page 52; 74pp; English.
 XX
 CC ICAM-1 and its functional derivs. are new. Also new are recombinant DNA
 CC able to express ICAM-1 or derivs. ICAM-1 is able to bind to a molecule
 CC present on the surface of lymphocytes and contains at least one of 17
 CC specified polypeptide sequences (see AAP80441-57). ICAM-1 is a 76-97KD
 CC glycoprotein which is a binding partner for LFA-1, and is involved in
 CC lymphocyte recognition and adhering to cell surfaces. ICAM-1 contains
 CC 5 Ig-like domains.
 CC
 SQ Sequence 5 AA:
 45.9%; Score 28; DB 10; Length 5;
 Query Match Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PRGGS 6
 | | | | |
 Db 1 prggs 5
 RESULT 8
 AAW70875
 ID AAW70875 standard; Peptide; 5 AA.
 XX AAW70875:
 02-MAR-1999 (first entry)
 DE ICAM-1 peptide fragment possibly recognised by LFA-1.
 XX
 KW Intracellular adhesion molecule; ICAM-1; LFA-1; Immune response;
 KW Inflammation; Lymphocyte function-associated antigen; tumour cell;
 KW metastasis; Binding ligand; detection; assay; peptide; polypeptide;
 KW Immune response; Inflammation; Immunosuppression.
 XX
 OS Mus musculus.
 XX
 PN US5831036-A.
 PD
 XX 03-NOV-1998.
 PD
 XX 25-OCT-1993; 93US-0140554.
 PF
 XX 27-APR-1990; 90US-0515478.
 PR 04-MAY-1987; 87US-0045963.
 PR 02-NOV-1987; 87US-0115798.
 PR 16-FEB-1988; 88US-0155943.
 PR 03-MAY-1988; 88US-0189815.
 PR 28-SEP-1988; 88US-0250446.
 PR 16-MAR-1989; 89US-0324481.
 PR 30-JUN-1989; 89US-0373882.
 PR 22-DEC-1989; 89US-0456647.
 PR 25-OCT-1993; 93US-0140554.
 XX
 PA (DAND) DANA FARBER CANCER INST INC.
 XX
 PI Dustin ML, Marlin SD, Rothlein R, Springer TA.
 XX
 DR WPI; 1998-609323/51.
 XX
 PT Soluble fragments of human inter-cellular adhesion molecule 1 -
 PT useful for inhibition of binding of leukocytes in immune responses
 PT e.g. organ transplantation
 XX
 PS Example 18; Column 47; 70pp; English.

CC ICAM-1 fragments obtained from recombinant expression of truncated
CC ICAM-1 coding sequences can be used in the control of adhesion
CC events in inflammatory conditions and immune responses. This is
CC achieved by the ICAM-1 fragments binding to and inhibiting the
CC action of leukocyte surface molecules e.g. LFA-1 which mediate
CC cell-cell adhesion events during immune responses. This inhibition
CC is useful for suppressing immune responses after organ
CC transplantation or skin grafting. Ligands derived from ICAM-1
CC which are possibly recognised by LFA-1 are described in GENESER
CC records AAW0872-W0880.
XX
SQ Sequence 5 AA;

Query Match 45.9%; Score 28; DB 14; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGS 6
| | | | |
DB 1 prgs 5

RESULT 9

ID AAR34037 standard; peptide; 6 AA.

AC AAR34037;

DT 06-AUG-1993 (first entry)

DE Peptide which binds the ICAM-1 binding site on IRBC.

KW Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC;
KW malaria; intercellular adhesion molecule; ICAM-1; CD54;
KW endothelial receptor; antibody.

PN W09306849-A.

PD 15-APR-1993.

PF 05-OCT-1992; 92WO-US08483.

PR 03-OCT-1991; 91US-0769625.

PR 03-APR-1992; 92US-0862708.

PR 12-JUN-1992; 92US-0899064.

XX (BLOO-) CENT BLOOD RES.

PA (USSA) US SEC OF ARMY.

DR WPI; 1993-134131/16.

PT Inhibition of CD36 binding to malaria infected erythrocytes - by
PT admin of CD36 or suitable fragment, antibody etc.; useful in
PT diagnosis and treatment of Plasmodium falciparum malaria

PS Disclosure; Page 46; 62pp; English.

CC The peptide AAR34037 is capable of binding the ICAM-1 binding site on
CC an IRBC. See related patents W09306848 and W09306850.

XX an IRBC. See related patents W09306848 and W09306850.

SQ Sequence 6 AA;

Query Match 45.9%; Score 28; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GGSVIV 9
| | | | |
DB 1 ggsviv 6

RESULT 10

ID AAR34089 standard; peptide; 6 AA.

AC AAR34089;

DT 06-AUG-1993 (first entry)

DE Peptide which binds the ICAM-1 binding site on IRBC.

KW Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC;
KW malaria; intercellular adhesion molecule; ICAM-1; CD54;
KW endothelial receptor; antibody.

OS Homo sapiens.

PN W09306850-A.

PD 15-APR-1993.

PF 05-OCT-1992; 92WO-US08484.

PR 03-OCT-1991; 91US-0769625.

PR 03-APR-1992; 92US-0862708.

PR 12-JUN-1992; 92US-0899063.

XX (BLOO-) CENT BLOOD RES.

PA (USSA) US SEC OF ARMY.

DR WPI; 1993-134132/16.

PT Inhibition of ICAM-1 binding to malaria-infected erythrocytes -
PT by admin. of ICAM-1 or fragment, antibody etc.; useful in
PT diagnosis or treatment of Plasmodium falciparum malaria

PS Claim 9; Page 49; 67pp; English.

CC The peptide AAR34089 is capable of binding the ICAM-1 binding site on
CC an IRBC. The sequence is shown as a pentapeptide GGSVIV in the
CC Claims but as the hexapeptide GGSVIV in the sequence listing.

CC See related patents W09306848 and W09306849.

XX Sequence 6 AA;

Query Match 45.9%; Score 28; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GGSVIV 9
| | | | |
DB 1 ggsviv 6

RESULT 11

ID AAW34379 standard; peptide; 7 AA.

AC AAW34379;

DT 04-MAR-1998 (first entry)

DE PKB substrate #26.

KW Protein kinase B; PKB; substrate; glycogen metabolism; pancreatic cancer;
KW regulator; protein synthesis; enzyme modulator; type II diabetes;
KW insulin-stimulated crosslink kinase; breast cancer; ovarian cancer;
KW therapy.

OS Synthetic.
 XX
 PN WO9722360-A2.
 XX
 PD 26-JUN-1997.
 XX
 PF 20-DEC-1996; 96WO-GB03186.
 XX
 PR 18-JUL-1996; 96GB-0015066.
 PR 20-DEC-1995; 95GB-0026083.
 PR 16-MAY-1996; 96GB-0010272.
 XX
 PA (MEDI-) MEDICAL RES COUNCIL.
 PA (UYDU-) UNIV DUNDEE.
 XX
 PI Alessi D, Cohen P, Cross D;
 XX
 DR WPI; 1997-341435/31.

Use of protein kinase B for regulation of glycogen metabolism and protein synthesis - also peptide substrates for PKB and methods for screening for modulators

Example 8; Page 58; 98pp; English.

This sequence represents a substrate for protein kinase B (PKB). The use of PKB, its analogues, isoforms, inhibitors, activators and/or functional equivalents for regulating glycogen metabolism and/or protein synthesis is the subject of the invention. This sequence can also be used in a method of the invention for identifying agents that modulate the activity of PKB. It can also be used to screen for modulators of enzymes that catalyse PKB phosphorylation. PKB (an insulin-stimulated crossinase kinase) and its analogues etc. are used to treat disease characterised by abnormal glycogen metabolism and/or protein synthesis, especially type II diabetes and cancer (specifically of breast, pancreas and ovary). The various screening methods are used to identify agents potentially useful for treating these diseases.

Sequence 7 AA;

Query Match 45.9%; Score 28; DB 18; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGS 6
 |||||
 2 prgs 6

RESULT 12

AAV63234
 ID AAV63234 standard; Peptide; 7 AA.

AAV63234;

02-MAR-2000 (first entry)

Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2718.

Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 inhibition; cadherin extracellular domain; cell adhesion recognition;
 OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
 cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 cadherin related neuronal receptor; Li-cadherin; protocadherin;
 desmoglein; desmocolin; calcium binding; cancer; tumour; obesity;
 rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 neurological disease; cyclic.

XX Synthetic.

OS Homo sapiens.

XX Key

Location/Qualifiers

FT Disulfide-bond 1..7
 XX
 PN WO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA00363.
 XX
 PR 05-MAY-1998; 98US-0073040.
 PR 06-NOV-1998; 98US-0187859.
 PR 20-JAN-1999; 99US-0234395.
 PR 08-MAR-1999; 99US-0264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI; 2000-038791/03.

New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological disease

Claim 84; Page 201; 252pp; English.

The present invention describes cadherin modulating agents (MA) comprising peptides which comprise a nonclassical cadherin cell adhesion recognition (CAR) sequence. The MA can be used for modulating nonclassical cadherin-mediated functions. They can be used for e.g. inhibiting adhesion of nonclassical-cadherin expressing cells in a mammal, enhancing delivery of a drug through the skin of a mammal, enhancing delivery of a drug to a tumor in a mammal, treating cancer in a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-expressing cell, preventing or treating obesity in a mammal, stimulating blood vessel regression in a mammal, enhancing drug delivery to the central nervous system, treating a demyelinating neurological disease, increasing vasopermeability in a mammal, enhancing adhesion of nonclassical cadherin-expressing cells, inhibiting synaptic stability in a mammal, or preventing pregnancy in a mammal. They can also be used for e.g. enhancing or directing neurite outgrowth, facilitating wound healing or reducing scar tissue, or enhancing adhesion of foreign tissue in a mammal. They can also be used for treating e.g. psoriasis, arthritis, age-related macular degeneration, multiple sclerosis and diabetes. The products can also be used for detection and diagnosis and in bioreactors. AAV60592 to AAV64572 represent specifically claimed peptides, and AAV64573 to AAV64643 and AA23183 to AA23186 represent sequences used in the exemplification of the present invention.

Sequence 7 AA;

Query Match 45.9%; Score 28; DB 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 IYTG 12
 |||||
 Db 3 lvtgc 7

RESULT 13

AAV63237
 ID AAV63237 standard; Peptide; 8 AA.

AAV63237;

02-MAR-2000 (first entry)

Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2721.

Modulation; nonclassical cadherin mediated cell adhesion; CAR;

KM inhibition; cadherin extracellular domain; cell adhesion recognition;
 KM OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
 KM cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KM cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KM desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KM rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KM neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX
 FT Key Location/Qualifiers
 FT Disulfide-bond 1..8
 XX
 XX MO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99MO-CA00363.
 XX
 XX 05-MAY-1998; 98US-0073040.
 PR 06-NOV-1998; 98US-0187859.
 XX 20-JAN-1999; 99US-0234395.
 XX 08-MAR-1999; 99US-0264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI: 2000-038791/03.
 XX
 PT New cadherin modulating agents, used for modulating nonclassical
 PT cadherin-mediated functions for treating e.g. cancers, obesity,
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
 PT disease
 PT
 PS Claim 84: Page 201: 252pp: English.
 XX
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue
 CC in a mammal. They can also be used for treating e.g. psoriasis,
 CC arthritis, age-related macular degeneration, multiple sclerosis and
 CC diabetes. The products can also be used for detection and diagnosis and
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed
 CC peptides, and AAY64573 to AAY64643 and AA233183 to AA233186 represent
 CC sequences used in the exemplification of the present invention.
 CC
 XX
 SQ Sequence 8 AA:

Query Match 45.9%; Score 28; DB 21; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 LVYGC 12
 |||||
 DB 4 lvcgc 8

RESULT 14
 ID AAY63240 standard; Peptide; 9 AA.
 AC AAY63240;
 XX
 DT 02-MAR-2000 (first entry)
 XX
 DE
 XX
 XX
 XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
 KM inhibition; cadherin extracellular domain; cell adhesion recognition;
 KM OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
 KM cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
 KM cadherin related neuronal receptor; Li-cadherin; protocadherin;
 KM desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
 KM rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
 KM neurological disease; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 FT Key Location/Qualifiers
 FT Disulfide-bond 1..9
 XX
 XX MO957149-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99MO-CA00363.
 XX
 XX 05-MAY-1998; 98US-0073040.
 PR 06-NOV-1998; 98US-0187859.
 XX 20-JAN-1999; 99US-0234395.
 XX 08-MAR-1999; 99US-0264516.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Gour BJ, Byers S;
 XX
 DR WPI: 2000-038791/03.
 XX
 PT New cadherin modulating agents, used for modulating nonclassical
 PT cadherin-mediated functions for treating e.g. cancers, obesity,
 PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
 PT disease
 PT
 PS Claim 84: Page 201: 252pp: English.
 XX
 XX The present invention describes cadherin modulating agents (MA)
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion
 CC recognition (CAR) sequence. The MAs can be used for modulating
 CC nonclassical cadherin-mediated functions. They can be used for e.g.
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
 CC mammal, enhancing delivery of a drug through the skin of a mammal,
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
 CC expressing cell, preventing or treating obesity in a mammal, stimulating
 CC blood vessel regression in a mammal, enhancing drug delivery to the
 CC central nervous system, treating a demyelinating neurological disease,
 CC increasing vasopermeability in a mammal, enhancing adhesion of
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound
 CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue
 CC in a mammal. They can also be used for treating e.g. psoriasis,
 CC arthritis, age-related macular degeneration, multiple sclerosis and
 CC diabetes. The products can also be used for detection and diagnosis and
 CC in bioreactors. AAY60592 to AAY64572 represent specifically claimed
 CC peptides, and AAY64573 to AAY64643 and AA233183 to AA233186 represent
 CC sequences used in the exemplification of the present invention.

XX Sequence 9 AA;
SQ
Query Match 45.9%; Score 28; DB 21; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 LVTGC 12
| | | | |
Db 5 lvtgc 9
RESULT 15
AAV63243
ID AAV63243 standard; Peptide: 10 AA.
AC AAV63243;
02-MAR-2000 (first entry)
Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2727.
DE
XX Modulation; nonclassical cadherin mediated cell adhesion; CAR;
KW Inhibition; cadherin extracellular domain; cell adhesion recognition;
KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8;
KW cadherin-12; cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
KW cadherin related neuronal receptor; Li-cadherin; protocadherin;
KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
KW neurological disease; cyclic.
XX Synthetic.
OS Homo sapiens.
OS
FH Key Location/Qualifiers
FT Disulfide-bond 1..10
PN WO957149-A2.
XX
PD 11-NOV-1999.
XX
PF 05-MAY-1999; 99WO-CA00363.
XX
PR 05-MAY-1998; 98US-0073040.
PR 06-NOV-1998; 98US-0187859.
PR 20-JAN-1999; 99US-0234395.
PR 08-MAR-1999; 99US-0264516.
PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
PI Blaschuk OW, Gour BJ, Byers S;
XX WPI; 2000-038791/03.
DR
XX
XX
PT New cadherin modulating agents, used for modulating nonclassical
PT cadherin-mediated functions for treating e.g. cancers, obesity,
PT rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
PT disease
PS
PS Claim 84; Page 201; 252pp; English.
XX
XX The present invention describes cadherin modulating agents (MA)
CC comprising peptides which comprise a nonclassical cadherin cell adhesion
CC recognition (CAR) sequence. The MAs can be used for modulating
CC nonclassical cadherin-mediated functions. They can be used for e.g.
CC inhibiting adhesion of nonclassical-cadherin expressing cells in a
CC mammal, enhancing delivery of a drug through the skin of a mammal,
CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in
CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting
CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-
CC expressing cell, preventing or treating obesity in a mammal, stimulating
CC blood vessel regression in a mammal, enhancing drug delivery to the

CC central nervous system, treating a demyelinating neurological disease,
CC increasing vasopermeability in a mammal, enhancing adhesion of
CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in
CC a mammal, or preventing pregnancy in a mammal. They can also be used for
CC e.g. enhancing or directing neurite outgrowth, facilitating wound
CC healing or reducing scar tissue, or enhancing adhesion of foreign tissue
CC in a mammal. They can also be used for treating e.g. psoriasis,
CC arthritis, age-related macular degeneration, multiple sclerosis and
CC diabetes. The products can also be used for detection and diagnosis and
CC in bioreactors. AAV60592 to AAV64572 represent specifically claimed
CC peptides, and AAV64573 to AAV64643 and AAZ33183 to AAZ33186 represent
CC sequences used in the exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 45.9%; Score 28; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 8 LVTGC 12
| | | | |
Db 6 lvtgc 10

Search completed: October 10, 2002, 06:16:25
Job time: 236 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 10, 2002, 06:20:47 : Search time 23.52 Seconds
(without alignments)
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Title: US-09-629-719D-8

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Total number of hits satisfying chosen parameters: 83765

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	83.6	11	2	US-08-789-078-9
2	51	83.6	11	2	US-08-752-633-9
3	51	83.6	11	5	PCT-US95-04886-9
4	45	73.8	12	2	US-08-789-078-7
5	45	73.8	12	2	US-08-789-078-8
6	45	73.8	12	2	US-08-752-633-7
7	45	73.8	12	2	US-08-752-633-8
8	45	73.8	12	3	US-08-844-978-4
9	45	73.8	12	3	US-08-844-978-7
10	45	73.8	12	5	PCT-US95-04886-7
11	45	73.8	12	5	PCT-US95-04886-8
12	28	45.9	5	6	US-09-187-859-2718
13	28	45.9	7	4	US-09-187-859-2721
14	28	45.9	8	4	US-09-187-859-2724
15	28	45.9	9	4	US-09-187-859-2727
16	28	45.9	10	4	US-09-187-859-2730
17	28	45.9	11	4	US-09-187-859-2733
18	27	44.3	10	3	US-08-925-002-7
19	27	44.3	12	3	US-09-100-409A-15
20	25	41.0	10	4	US-08-847-844A-38
21	24	39.3	7	4	US-09-187-859-1595
22	24	39.3	8	4	US-09-187-859-1596
23	24	39.3	9	4	US-08-258-754-122
24	24	39.3	9	4	US-09-042-107-122
25	24	39.3	9	4	US-09-187-859-1597
26	24	39.3	10	1	US-08-525-584-3
27	24	39.3	10	2	US-08-789-078-13

28	24	39.3	10	2	US-08-752-633-13	Sequence 13, Appl
29	24	39.3	10	4	US-09-187-859-1600	Sequence 1600, Ap
30	24	39.3	10	5	PCT-US95-04886-13	Sequence 13, Appl
31	24	39.3	11	4	US-08-602-999A-260	Sequence 260, App
32	24	39.3	11	4	US-09-478-479B-26	Sequence 26, Appl
33	24	39.3	11	4	US-09-187-859-1603	Sequence 1603, Ap
34	24	39.3	12	2	US-08-789-078-15	Sequence 14, Appl
35	24	39.3	12	2	US-08-789-078-15	Sequence 15, Appl
36	24	39.3	12	2	US-08-752-633-14	Sequence 14, Appl
37	24	39.3	12	2	US-08-752-633-15	Sequence 15, Appl
38	24	39.3	12	3	US-08-844-978-3	Sequence 3, Appl
39	24	39.3	12	3	US-08-844-978-6	Sequence 6, Appl
40	24	39.3	12	4	US-09-426-680-3	Sequence 3, Appl
41	24	39.3	12	4	US-09-344-456-2	Sequence 2, Appl
42	24	39.3	12	5	PCT-US95-04886-14	Sequence 14, Appl
43	24	39.3	12	5	PCT-US95-04886-15	Sequence 15, Appl
44	23	37.7	7	3	US-09-150-133-45	Sequence 45, Appl
45	23	37.7	7	3	US-09-150-141-45	Sequence 45, Appl

ALIGNMENTS

RESULT 1
US-08-789-078-9
Sequence 9, Application US/08789078
Patent No. 5843885
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Sahaan, Teruna
APPLICANT: Chan, Marcia
APPLICANT: Tibbels, Scott
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
TITLE OF INVENTION: IMMUNE TOLERANCE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,078
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,513
FILING DATE: 19-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: T-cell

CELL LINE: HL-60
US-08-789-078-9

Query Match

Best Local Similarity 83.6%; Score 51; DB 2; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGGSVLTG 11
|||||
Db 2 PRGGSVLTG 11

RESULT 2

US-08-752-633-9
; Sequence 9, Application US/08752633
; Patent No. 5863885

GENERAL INFORMATION:

APPLICANT: Benedict, Stephen H.

APPLICANT: Shahan, Teruna

APPLICANT: Chan, Marcia

TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

STREET: 1101 Walnut St.

CITY: Kansas City

STATE: MO

COUNTRY: USA

ZIP: 64106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/752,633

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRATION NUMBER: 26262

REFERENCE/DOCKET NUMBER: 22833

TELECOMMUNICATION INFORMATION:

TELEPHONE: (816)474-9050

TELEFAX: (816)474-9057

TELEX: 434-363

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: T-cell

CELL LINE: HL-60

US-08-752-633-9

Query Match

Best Local Similarity 83.6%; Score 51; DB 2; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGGSVLTG 11
|||||
Db 2 PRGGSVLTG 11

RESULT 3

PCT-US95-04886-9

; Sequence 9, Application PC/TUS9504886

GENERAL INFORMATION:

APPLICANT: Benedict, Stephen H.

APPLICANT: Shahan, Teruna

APPLICANT: Chan, Marcia

TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

STREET: 1101 Walnut St.

CITY: Kansas City

STATE: MO

COUNTRY: USA

ZIP: 64106

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/04886

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Collins, John M.

REGISTRATION NUMBER: 26262

REFERENCE/DOCKET NUMBER: 22833

TELECOMMUNICATION INFORMATION:

TELEPHONE: (816)474-9050

TELEFAX: (816)474-9057

TELEX: 434-363

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

CELL TYPE: T-cell

CELL LINE: HL-60

PCT-US95-04886-9

Query Match

Best Local Similarity 83.6%; Score 51; DB 5; Length 11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGGSVLTG 11
|||||
Db 2 PRGGSVLTG 11

RESULT 4

US-08-789-078-7

; Sequence 7, Application US/08789078

Patent No. 5843885

GENERAL INFORMATION:

APPLICANT: Benedict, Stephen H.

APPLICANT: Shahan, Teruna

APPLICANT: Chan, Marcia

TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS

STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,078
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,513
FILING DATE: 19-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ. ID NO.: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: T-cell
CELL LINE: HL-60
US-08-789-078-7

Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGGSVLT 10
Db 3 PRGGSVLT 11

RESULT 5
Sequence 8, Application US/08789078
Patent No. 5843885
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Slahaan, Teruna
APPLICANT: Chan, Marcia
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
TITLE OF INVENTION: IMMUNE TOLERANCE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,078
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/229,513
FILING DATE: 19-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ. ID NO.: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: cyclic
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: T-cell
CELL LINE: HL-60
US-08-789-078-8

Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGGSVLT 10
Db 3 PRGGSVLT 11

RESULT 6
US-08-752-633-7
Sequence 7, Application US/08752633
Patent No. 5863889
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Slahaan, Teruna
APPLICANT: Chan, Marcia
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
TITLE OF INVENTION: IMMUNE TOLERANCE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,633
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050

TELEFAX: 816/474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: internal
ORGANISM: Homo sapiens
CELL TYPE: T-cell
CELL LINE: HL-60
US-08-752-633-7

Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRGGSVLT 10
Db 3 PRGGSVLT 11

RESULT 7
US-08-752-633-8
Sequence 8, Application US/08752633
Patent No. 5863889
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Slahaan, Teruna
APPLICANT: Chan, Marcia
APPLICANT: Tibbets, Scott
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,633
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816/474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: cyclic
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE: internal
ORGANISM: Homo sapiens
CELL TYPE: T-cell

CELL LINE: HL-60
US-08-752-633-8

Query Match 73.8%; Score 45; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRGGSVLT 10
Db 3 PRGGSVLT 11

RESULT 8
US-08-844-978-4
Sequence 4, Application US/08844978
Patent No. 6075004
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen
APPLICANT: Slahaan, Teruna
APPLICANT: Chan, Marcia
APPLICANT: Tibbets, Scott
TITLE OF INVENTION: Peptide Compositions Which Induce Immune
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,978
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 24769-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: 816/474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-844-978-4

Query Match 73.8%; Score 45; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PRGGSVLT 10
Db 3 PRGGSVLT 11

RESULT 9
US-08-844-978-7
Sequence 7, Application US/08844978
Patent No. 6075004
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen
APPLICANT: Slahaan, Teruna

APPLICANT: Chan, Marcia
APPLICANT: Tibbetts, Scott
TITLE OF INVENTION: Peptide Compositions which Induce Immune
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2405 Grand Boulevard, Suite 400
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/844,978
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 24769-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-844-978-7

Query Match 73.8%; Score 45; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGGSVLVT 10
|||||
DB 3 PRGGSVLVT 11

RESULT 10
PCT-US95-04886-7
Sequence 7, Application PC/TUS9504886
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Siahaan, Teruna
APPLICANT: Chan, Marcia
APPLICANT: Tibbetts, Scott
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04886
FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: T-cell
CELL LINE: HL-60
PCT-US95-04886-7

Query Match 73.8%; Score 45; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 PRGGSVLVT 10
|||||
DB 3 PRGGSVLVT 11

RESULT 11
PCT-US95-04886-8
Sequence 8, Application PC/TUS9504886
GENERAL INFORMATION:
APPLICANT: Benedict, Stephen H.
APPLICANT: Siahaan, Teruna
APPLICANT: Chan, Marcia
APPLICANT: Tibbetts, Scott
TITLE OF INVENTION: ICAM-1/LFA-1 PEPTIDES FOR INDUCING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 1101 Walnut St.
CITY: Kansas City
STATE: MO
COUNTRY: USA
ZIP: 64106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04886
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Collins, John M.
REGISTRATION NUMBER: 26262
REFERENCE/DOCKET NUMBER: 22833
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816)474-9050
TELEFAX: (816)474-9057
TELEX: 434-363
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: cyclic
MOLECULE TYPE: peptide

HYPOTHETICAL: NO
FRAGMENT TYPE: Internal
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
CELL TYPE: T-cell
CELL LINE: HL-60
PCT-US95-04886-8

Query Match 73.8%; Score 45; DB 5; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRGGSVLT 10
Db 3 PRGGSVLT 11

RESULT 12
Patent No. 5284931
APPLICANT: SPRINGER, TIMOTHY A.; ROTHLEIN, ROBERT; MARLIN,
STEVEN D.; DUSTIN, MICHAEL L.
TITLE OF INVENTION: INTERCELLULAR ADHESION MOLECULES AND
THEIR BINDING LIGANDS
NUMBER OF SEQUENCES: 41
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/515,478
FILING DATE: 27-APR-1990
SEQ ID NO: 12
LENGTH: 5
5284931-12

Query Match 45.9%; Score 28; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 PRGGS 6
Db 1 PRGGS 5

RESULT 13
US-09-187-859-2718
Sequence 2718, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2718
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2718

Query Match 45.9%; Score 28; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LVYGC 12
|||||

Db 3 LVYGC 7

RESULT 14
US-09-187-859-2721
Sequence 2721, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2721
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2721

Query Match 45.9%; Score 28; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LVYGC 12
Db 4 LVYGC 8

RESULT 15
US-09-187-859-2724
Sequence 2724, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gour, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100086.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 2724
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: Protocadherin cell adhesion recognition sequence
US-09-187-859-2724

Query Match 45.9%; Score 28; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 LVYGC 12
Db 5 LVYGC 9

Search completed: October 10, 2002, 06:20:47
Job time: 368 sec